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πάντα ρὲι — Everything Flows

Editorial*

Things are the way they are because they got that way. This is a folksy summary of an important insight: that in order to understand the present, we must know how it developed over time. If we want to truly appreciate human diversity, we need to know how it developed over time: how past people lived, how their mentalities and cultures kept changing, how their physical and genetic constitution changed, and how earlier populations were absorbed or exterminated by foreign invaders. Ethnogenesis, balanced by the merging or extinction of nations, has been a continuous process that we can still observe in our time.

For the historical period we have, by definition, written records as our main source of information. For prehistory, we depend on archaeology — and on linguistics. Even when we have no written records from the past, we can use the comparative method to detect similarities between existing languages. Such similarities can have two possible origins: They can be the result of shared descent from an ancestral language — and physical descent from the speakers of that ancestral language — or they can be the result of borrowing where words and sometimes grammatical elements move from one language to another. In the first case we speak of a language family, in the second of a *Sprachenbund* (German, literally "language federation").

The study of the Indo-European language family began in the late 18th century with the work of the British lawyer and philologist William Jones. After becoming a judge at the High Court in Calcutta, Jones began learning Sanskrit, the sacred language of the Vedas, spoken most likely by invading Aryan tribes in the late 2nd millennium BC. He noticed something entirely unexpected: similarities between Sanskrit, Latin, and classical Greek. He also noted: "there is a similar reason, though not quite as forcible, for supposing that both the Gothic and the Celtic, though blended with a very different idiom, had the same origin with the Sanskrit; and the old Persian might be added to the same family..." (cited from Renfrew, 1990, p. 9). Jones concluded correctly that there must have been an ancient people that split up in prehistoric times, carrying versions of its language to places as distant as Europe and India.

But where did these first Indo-Europeans live? Although some 19th-century scholars had already proposed a Steppe pastoralist origin of the proto-Indo-Europeans, the more common view until the mid-20th century was a Northern European origin, with North-to-South migrations similar to those of the 5th and 6th centuries AD, when roving Germanic tribes invaded the carcass of the former Roman Empire. Eventually, the Northern European theory was forcefully challenged by Lithuanian archaeologist Marija Gimbutas (1956). In her kurgan theory, she proposed that the first Indo-Europeans were the people of an Early Bronze Age pastoralist culture in the Steppe north of the Black Sea and the Caspian Sea that was characterized by its distinctive burial mounds (kurgans).

The kurgan theory, in turn, was challenged by Colin Renfrew (1990), who postulated that Anatolian farmers, whose agricultural lifestyle gave them a demographic advantage over native European hunter-gatherers, carried the Indo-European languages into Europe. This theory was supported by early genetic evidence of a South-East to North-West gradient throughout most of Europe (Cavalli-Sforza et al., 1994).

The controversy was resolved only in the 21st century, when the sequencing of ancient genomes from archaeological sites demonstrated the large-scale though incomplete replacement of Neolithic Northern European populations by invaders from the Pontic-Caspian Steppe at the beginning of the 3rd millennium BC (Haak et al., 2015). This finding supported Gimbutas' theory and agreed with archaeological evidence about the spread of the Corded Ware culture in Central Europe and somewhat later the Bell Beaker culture in Western Europe.

This stage of research, where ancient DNA is used to track ancient migrations and population replacements, is now being followed up by a different kind of studies that seek to determine not only the

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genetic affiliations of bones unearthed from archaeological sites, but also their genetic traits. One example of this new research program is an article by Davide Piffer in this issue of *Mankind Quarterly*. It examines polygenic scores for a number of traits in 414 published and publicly accessible genomes from archaeological sites in Eastern Europe and adjacent regions, plus modern European genomes from the 1000Genomes project for comparison. The main question that this article seeks to answer is: Why were the Yamnaya (Gimbutas' kurgan people) so successful? Did they possess genetic traits that helped them to multiply and to displace other, competing populations, spreading their language and their genes over vast territories?

Virtually all important human traits show highly polygenic inheritance, which means they are each influenced by polymorphisms (genetic variations) in hundreds or thousands of different genes. Therefore, the author did not study individual polymorphisms. He rather calculated polygenic scores based on published genome-wide association studies for traits such as height, skin colour, educational attainment, and some psychological and psychiatric traits. The amount of information he obtained is staggering. He first used admixture analysis, demonstrating that the Yamnaya were not genetically unique. They rather were a blend of several earlier groups, with names such as Steppe Pastoralist and Eastern Hunter-Gatherer. This emphasizes the role of genetic admixture in the formation of ethno-linguistic groups.

Another take-home message is that human evolution is an ongoing process. Comparing ancient and modern populations, the results show for example that genetic predispositions to educational attainment and autism increased, confirming earlier observations (Piffer, 2025; Piffer & Kirkegaard, 2024), while genetic susceptibility to some other psychiatric traits is lower today than it was in prehistoric times.

Results of this kind also speak to another old controversy: the importance of group selection for human evolution. Did polygenic predispositions to traits such as educational attainment, height or skin colour change over time because natural selection was acting on individuals manifesting these traits? Or did they change because populations with certain genetic predispositions replaced other populations? Did, for example, populations with polygenic predisposition to higher intelligence exterminate and replace populations with lower intelligence polygenic scores? This would be group selection.

The study of ancient DNA has so far been applied to polygenic evolution taking place on time scales of some millennia. Presumably, larger sample sizes would be needed to study evolutionary trends in younger populations on time scales of centuries rather than millennia, for example in Christian Europe or the Muslim Middle East from the Middle Age to the Industrial Revolution. The study of selection in present-day populations, by contrast, is low-hanging fruit. All we need to do is to relate polygenic scores of post-reproductive living individuals to their lifetime reproductive output. This allows us to predict the genetic predispositions of future generations (e.g., Hugh-Jones & Abdellaoui, 2022).

The new applications of molecular genetics to human history and prehistory all converge on the same conclusion: Everything flows, as has already been stated by Heraclitus of Ephesus two and a half millennia ago. The earlier scholarly doctrine that human cultures keep changing but human genetics and with it "human nature" is frozen in time needs to be discarded. For example, until the late 20th century many scholars believed that the presently living human races are nearly immutable. They were thought to have evolved from various regional populations of *Homo erectus* over the last 500,000 years, a time scale too long to be interesting for students of history and late prehistory.

This earlier "multiregional" theory was snuffed out only toward the end of the 20th century when studies of mitochondrial DNA found a recent origin of "mitochondrial Eve", and a similarly recent date was soon found also for the Y chromosome. At that point it became undeniable that modern humans had a recent African origin and the present human races evolved only after the African exodus of anatomically modern humans about 60,000 years ago. Nevertheless, as late as 2005, a commentator in *Science* magazine asked: "Are humans still evolving?" (Balter, 2005). Today this question is even more absurd than it was 20 years ago, at least to those familiar with the science. How could anybody ever believe that through some kind of magic, humans had stopped evolving in early prehistoric times?

Perhaps the reason for the tenacious belief in human genetic immutability, without any good evidence and contrary to all we know about how evolution and genetics work, is the desire to feel safe in a thoroughly predictable, stable, unchanging world. In the absence of reality checks, humans are inclined to believe whatever makes them feel good, evidence be damned, as demonstrated by the popularity of traditional religions and of the post-religious ideologies of educated people in the postmodern West. There could be a more specific reason why many knowledgeable people recoil from the inquiry into ongoing human evolution. Some seriously ill patients are reluctant to go to the doctor for fear of what the doctor may tell them. It might be an illness with a "guarded" prognosis — a medical euphemism meaning the patient is going to die. When Hugh-Jones and Abdellaoui (2022) studied ongoing polygenic evolution in the British population, their main finding was strong selection against genetic variants associated with higher educational attainment — implying a guarded prognosis for British society and the British nation.

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